



Figures

**Figure 1 - Nucleotide and protein sequence of *Aspergillus ochraceus* II
alpha hydroxylase**

5	tggaagtttt tacacttatt atgccggagc cgaagaattc tgagtcgagg gggtggggaa	60
	caacactata agacctacaa ccacttggat ttggtgaatt tacacgggca ttatcaaaac	120
	agccacaagc tgacagctca ttatc atg ccc ttc ttc act ggg ctt ctg gcg	172
	Met Pro Phe Phe Thr Gly Leu Leu Ala	
10		
	att tac cat agt ctc ata ctc gac aac cca gtc caa acc ctg agc acc	220
	Ile Tyr His Ser Leu Ile Leu Asp Asn Pro Val Gln Thr Leu Ser Thr	
	10 15 20 25	
15	att gtc gta ttg gcg gca gcg tac tgg ctc gca acg ctc cag ccg agc	268
	Ile Val Val Leu Ala Ala Tyr Trp Leu Ala Thr Leu Gln Pro Ser	
	30 35 40	
20	gac ctt cct gag ctg aat ccc gcc aaa cca ttc gag ttc acc aat cgt	316
	Asp Leu Pro Glu Leu Asn Pro Ala Lys Pro Phe Glu Phe Thr Asn Arg	
	45 50 55	
25	cgt cgt gtt cat gag ttt gtt gaa aat agt aag agc ttg ctt gct cgg	364
	Arg Arg Val His Glu Phe Val Glu Asn Ser Lys Ser Leu Leu Ala Arg	
	60 65 70	
30	ggg agg gaa ttg cac ggg cac gag ccg tac aga ctc atg tct gaa tgg	412
	Gly Arg Glu Leu His Gly His Glu Pro Tyr Arg Leu Met Ser Glu Trp	
	75 80 85	
35	gga tcc ttg att gtc ctg ccc cca gag tgc gcc gac gag ctg cgc aac	460
	Gly Ser Leu Ile Val Leu Pro Pro Glu Cys Ala Asp Glu Leu Arg Asn	
	90 95 100 105	
40	gac cca aga atg gac ttt gag acg ccc acc acc gac gac tcc cac gga	508
	Asp Pro Arg Met Asp Phe Glu Thr Pro Thr Thr Asp Asp Ser His Gly	
	110 115 120	
45	tat atc cct ggc ttc gac gct ctc aac gca gac ccg aac ctg act aaa	556
	Tyr Ile Pro Gly Phe Asp Ala Leu Asn Ala Asp Pro Asn Leu Thr Lys	
	125 130 135	
50	gtg gtc acc aag tac ctc aca aaa gca ttg aac aag ctt act gct ccg	604
	Val Val Thr Lys Tyr Leu Thr Lys Ala Leu Asn Lys Leu Thr Ala Pro	
	140 145 150	
55	atc tcg cat gaa gcg tcc atc gcc atg aaa gcg gtg ctg ggt gac gat	652
	Ile Ser His Glu Ala Ser Ile Ala Met Lys Ala Val Leu Gly Asp Asp	
	155 160 165	
60	cca gat tgg cgt gag atc tac cca gcc aga gac ttg ctc cag ctc gtc	700
	Pro Asp Trp Arg Glu Ile Tyr Pro Ala Arg Asp Leu Leu Gln Leu Val	
	170 175 180 185	
65	gcc cgg atg tcg aca aga gtg ttc ctt gcc gag gaa atg tgc aat aac	748
	Ala Arg Met Ser Thr Arg Val Phe Leu Gly Glu Glu Met Cys Asn Asn	
	190 195 200	
70	cag gat tgg atc caa acc tca tca caa tac gcg gcc ctt gcc ttc ggt	796
	Gln Asp Trp Ile Gln Thr Ser Ser Gln Tyr Ala Ala Leu Ala Phe Gly	
	205 210 215	
75	gtc ggt gac aag ctt aga ata tac ccg aga atg atc aga ccg ata gta	844
	Val Gly Asp Lys Leu Arg Ile Tyr Pro Arg Met Ile Arg Pro Ile Val	
	220 225 230	
80	cat tgg ttc atg cca tcc tgt tgg gag ctg cgc cga tcg ctg cga cgc	892
	His Trp Phe Met Pro Ser Cys Trp Glu Leu Arg Ser Leu Arg Arg	
	235 240 245	
85	tgc cga cag att ctc acg ccg tac att cac aaa cgc aag tcc ctg aag	940
	Cys Arg Gln Ile Leu Thr Pro Tyr Ile His Lys Arg Lys Ser Leu Lys	
	250 255 260 265	

Figure 1, continued

1	ggg acc acg gac gag cag ggc aag ccc ctt atg ttt gat gat tcc atc Gly Thr Thr Asp Glu Gln Gly Lys Pro Leu Met Phe Asp Asp Ser Ile 270 275 280	988
5	gag tgg ttc gag cga gag ctg ggt ccc aac cac gac gcg gtc ctg aag Glu Trp Phe Glu Arg Glu Leu Gly Pro Asn His Asp Ala Val Leu Lys 285 290 295	1036
10	cag gtc acg ctc tcc ata gtt gct atc cac acc acg agt gac cta ctc Gln Val Thr Leu Ser Ile Val Ala Ile His Thr Thr Ser Asp Leu Leu 300 305 310	1084
15	ttg cag gcc atg agc gat ctc gcg cag aac ccg aaa gtg cta caa gca Leu Gln Ala Met Ser Asp Leu Ala Gln Asn Pro Lys Val Leu Gln Ala 315 320 325	1132
20	gtg cgc gag gag gtg gtc cga gtg ctg agc acc gag ggg ctc agc aag Val Arg Glu Glu Val Val Arg Val Leu Ser Thr Glu Gly Leu Ser Lys 330 335 340 345	1180
25	gtc tcg ctt cac agt ctc aag ctc atg gac agc gcg ttg aag gaa agc Val Ser Leu His Ser Leu Lys Leu Met Asp Ser Ala Leu Lys Glu Ser 350 355 360	1228
30	cag cgt ctc agg cct acg ctt ctc ggc tcc ttt cgt cgg cag gca acg Gln Arg Leu Arg Pro Thr Leu Leu Gly Ser Phe Arg Arg Gln Ala Thr 365 370 375	1276
35	aat gac atc aag ctg aag agc ggg ttt gtc ata aag aaa ggg act aga Asn Asp Ile Lys Leu Lys Ser Gly Phe Val Ile Lys Lys Gly Thr Arg 380 385 390	1324
40	gtc gtg atc gac agc acc cat atg tgg aat ccc gag tat tac act gac Val Val Ile Asp Ser Thr His Met Trp Asn Pro Glu Tyr Tyr Thr Asp 395 400 405	1372
45	cct ctc cag tac gac ggg tac cgc tac ttc aac aag cgg cag aca ccc Pro Leu Gln Tyr Asp Gly Tyr Arg Tyr Phe Asn Lys Arg Gln Thr Pro 410 415 420 425	1420
50	ggc gag gac aag aac gcg ttg ctc gtc agc aca agc gcc aac cac atg Gly Glu Asp Lys Asn Ala Leu Leu Val Ser Thr Ser Ala Asn His Met 430 435 440	1468
55	gga ttc ggt cac ggc gtt cac gcc tgt cct ggc aga ttc ttc gcc tcc Gly Phe Gly His Gly Val His Ala Cys Pro Gly Arg Phe Phe Ala Ser 445 450 455	1516
60	aac gag atc aag att gcc ttg tgt cat atc atc tta aat tat gag tgg Asn Glu Ile Lys Ile Ala Leu Cys His Ile Ile Leu Asn Tyr Glu Trp 460 465 470	1564
65	cgt ctt cca gac ggc ttc aag ccc cag cct ctc aac atc ggg atg act Arg Leu Pro Asp Gly Phe Lys Pro Gln Pro Leu Asn Ile Gly Met Thr 475 480 485	1612
70	tat ctg gcg gat ccc aat acc agg atg ctg atc agg cca cgc aag gcg Tyr Leu Ala Asp Pro Asn Thr Arg Met Leu Ile Arg Pro Arg Lys Ala 490 495 500 505	1660
75	gag atc gat atg gcg agt tta act gtg tag gtcgaacacg aagtcctgat Glu Ile Asp Met Ala Ser Leu Thr Val *	1710
80	gaagtgttat tggtcagtgg gtgaagcaag tcgcagaaat gtgtaacaat ttataagaat aaaaaa	1770 1776

Figure 2 - Nucleotide and protein sequence of human oxidoreductase

5	atg gga gac tcc cac gtg gac acc agc tcc acc gtg tcc gag gcg gtg Met Gly Asp Ser His Val Asp Thr Ser Ser Thr Val Ser Glu Ala Val	48
10	gcc gaa gaa gta tct ctt ttc agc atg acg gac atg att ctg ttt tcg Ala Glu Glu Val Ser Leu Phe Ser Met Thr Asp Met Ile Leu Phe Ser	96
15	ctc atc gtg ggt ctc cta acc tac tgg ttc ctc ttc aga aag aaa aaa Leu Ile Val Gly Leu Leu Thr Tyr Trp Phe Leu Phe Arg Lys Lys Lys	144
20	gaa gaa gtc ccc gag ttc acc aaa att cag aca ttg acc tcc tct gtc Glu Glu Val Pro Glu Phe Thr Lys Ile Gln Thr Leu Thr Ser Ser Val	192
25	aga gag agc agc ttt gtg gaa aag atg aag aaa acg ggg agg aac atc Arg Glu Ser Ser Phe Val Glu Lys Met Lys Lys Thr Gly Arg Asn Ile	240
30	atc gtg ttc tac ggc tcc cag acg ggg act gca gag gag ttt gcc aac Ile Val Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Glu Phe Ala Asn	288
35	cgc ctg tcc aag gac gcc cac cgc tac ggg atg cga ggc atg tca gcg Arg Leu Ser Lys Asp Ala His Arg Tyr Gly Met Arg Gly Met Ser Ala	336
40	gac cct gag gag tat gac ctg gcc gac ctg agc agc ctg cca gag atc Asp Pro Glu Glu Tyr Asp Leu Ala Asp Leu Ser Ser Leu Pro Glu Ile	384
45	gac aac gcc ctg gtg gtt ttc tgc atg gcc acc tac ggt gag gga gac Asp Asn Ala Leu Val Val Phe Cys Met Ala Thr Tyr Gly Glu Gly Asp	432
50	ccc acc gac aat gcc cag gac ttc tac gac tgg ctg cag gag aca gac Pro Thr Asp Asn Ala Gln Asp Phe Tyr Asp Trp Leu Gln Glu Thr Asp	480
55	gtg gat ctc tct ggg gtc aag ttc gcg gtg ttt ggt ctt ggg aac aag Val Asp Leu Ser Gly Val Lys Phe Ala Val Phe Gly Leu Gly Asn Lys	528
60	acc tac gag cac ttc aat gcc atg ggc aag tac gtg gac aag cgg ctg Thr Tyr Glu His Phe Asn Ala Met Gly Lys Tyr Val Asp Lys Arg Leu	576
65	gag cag ctc ggc gcc cag cgc atc ttt gag ctg ggg ttg ggc gac gac Glu Gln Leu Gly Ala Gln Arg Ile Phe Glu Leu Gly Leu Gly Asp Asp	624
70	gat ggg aac ttg gag gag gac ttc atc acc tgg cga gag cag ttc tgg Asp Gly Asn Leu Glu Glu Asp Phe Ile Thr Trp Arg Glu Gln Phe Trp	672
75	ccg gcc gtg tgt gaa cac ttt ggg gtg gaa gcc act ggc gag gag tcc Pro Ala Val Cys Glu His Phe Gly Val Glu Ala Thr Gly Glu Glu Ser	720
80	agc att cgc cag tac gag ctt gtg gtc cac acc gac ata gat gcg gcc Ser Ile Arg Gln Tyr Glu Leu Val Val His Thr Asp Ile Asp Ala Ala	768
85	aag gtg tac atg ggg gag atg ggc cgg ctg aag agc tac gag aac cag Lys Val Tyr Met Gly Glu Met Gly Arg Leu Lys Ser Tyr Glu Asn Gln	816
90	aag ccc ccc ttt gat gcc aag aat ccg ttc ctg gct gca gtc acc acc Lys Pro Pro Phe Asp Ala Lys Asn Pro Phe Leu Ala Ala Val Thr Thr	864
95	aac cgg aag ctg aac cag gga acc gag cgc cac ctc atg cac ctg gaa Asn Arg Lys Leu Asn Gln Gly Thr Glu Arg His Leu Met His Leu Glu	912
100	ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtg	960

Figure 2, continued

	ttg gac atc tcg gac tcc aaa atc agg tat gaa tct ggg gac cac gtg	960
5	Leu Asp Ile Ser Asp Ser Lys Ile Arg Tyr Glu Ser Gly Asp His Val 305 310 315 320	
	gct gtg tac cca gcc aac gac tct gct ctc gtc aac cag ctg ggc aaa Ala Val Tyr Pro Ala Asn Asp Ser Ala Leu Val Asn Gln Leu Gly Lys 325 330 335	1008
10	atc ctg ggt gcc gac ctg gac gtc gtc atg tcc ctg aac aac ctg gat Ile Leu Gly Pro Ala Asp Leu Asp Val Met Ser Leu Asn Asn Leu Asp 340 345 350	1056
15	gag gag tcc aac aag aag cac cca ttc ccg tgc cct acg tcc tac cgc Glu Glu Ser Asn Lys Lys His Pro Phe Pro Cys Pro Thr Ser Tyr Arg 355 360 365	1104
20	acg gcc ctc acc tac tac ctg gac atc acc aac ccg ccg cgt acc aac Thr Ala Leu Thr Tyr Tyr Leu Asp Ile Thr Asn Pro Pro Arg Thr Asn 370 375 380	1152
25	gtg ctg tac gag ctg gcg cag tac gcc tcg gag ccc tcg gag cag gag Val Leu Tyr Glu Leu Ala Gln Tyr Ala Ser Glu Pro Ser Glu Gln Glu 385 390 395 400	1200
30	ctg ctg cgc aag atg gcc tcc tcc tcc ggc gag ggc aag gag ctg tac Leu Leu Arg Lys Met Ala Ser Ser Ser Gly Glu Gly Lys Glu Leu Tyr 405 410 415	1248
	ctg agc tgg gtg gtg gag gcc ccg agg cac atc ctg gcc atc ctg cag Leu Ser Trp Val Val Glu Ala Arg Arg His Ile Leu Ala Ile Leu Gln 420 425 430	1296
35	gac tgc ccg tcc ctg ccg ccc ccc atc gac cac ctg tgt gag ctg ctg Asp Cys Pro Ser Leu Arg Pro Pro Ile Asp His Leu Cys Glu Leu Leu 435 440 445	1344
40	ccg cgc ctg cag gcc cgc tac tac tcc atc gcc tca tcc tcc aag gtc Pro Arg Leu Gln Ala Arg Tyr Tyr Ser Ile Ala Ser Ser Ser Lys Val 450 455 460	1392
45	cac ccc aac tct gtg cac atc tgt gcg gtg gtt gtg gag tac gag acc His Pro Asn Ser Val His Ile Cys Ala Val Val Val Glu Tyr Glu Thr 465 470 475 480	1440
50	aag gcc ggc cgc atc aac aag ggc gtg gcc acc aac tgg ctg ccg gcc Lys Ala Gly Arg Ile Asn Lys Gly Val Ala Thr Asn Trp Leu Arg Ala 485 490 495	1488
	aag gag cct gcc ggg gag aac ggc ggc cgt gcg ctg gtg ccc atg ttc Lys Glu Pro Ala Gly Glu Asn Gly Arg Ala Leu Val Pro Met Phe 500 505 510	1536
55	gtg cgc aag tcc cag ttc cgc ctg ccc ttc aag gcc acc acg cct gtc Val Arg Lys Ser Gln Phe Arg Leu Pro Phe Lys Ala Thr Thr Pro Val 515 520 525	1584
60	atc atg gtg ggc ccc gcc acc ggg gtg gca ccc ttc ata ggc ttc atc Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Ile Gly Phe Ile 530 535 540	1632
65	cag gag ccg gcc tgg ctg cga cag cag ggc aag gag gtg ggg gag acg Gln Glu Arg Ala Trp Leu Arg Gln Gln Gly Lys Glu Val Gly Glu Thr 545 550 555 560	1680
70	ctg ctg tac tac ggc tgc cgc cgc tcg gat gag gac tac ctg tac cgc Leu Leu Tyr Tyr Gly Cys Arg Arg Ser Asp Glu Asp Tyr Leu Tyr Arg 565 570 575	1728
	gag gag ctg gcg cag ttc cac agg gac ggt gcg ctc acc cag ctc aac Glu Glu Leu Ala Gln Phe His Arg Asp Gly Ala Leu Thr Gln Leu Asn 580 585 590	1776
75	gtg gcc ttc tcc ccg gag cag tcc cac aag gtc tac gtc cag cac ctg Val Ala Phe Ser Arg Glu Gln Ser His Lys Val Tyr Val Gln His Leu 595 600 605	1824
80	cta aag caa gac cga gag cac ctg tgg aag ttg atc gaa ggc ggt gcc Leu Lys Gln Asp Arg Glu His Leu Trp Lys Leu Ile Glu Gly Gly Ala 610 615 620	1872

Figure 2, continued

	610	615	620	
	cac atc tac gtc tgt	ggg gat gca cgg aac atg	gcc agg gat gtg cag	1920
	His Ile Tyr Val Cys	Gly Asp Ala Arg Asn Met	Ala Arg Asp Val Gln	
5	625	630	635	640
	aac acc ttc tac gac	atc gtg gct gag ctc	ggg gcc atg gag cac gcg	1968
	Asn Thr Phe Tyr Asp	Ile Val Ala Glu Leu	Gly Ala Met Glu His Ala	
10		645	650	655
	cag gcg gtg gac tac	atc aag aaa ctg atg	acc aag ggc cgc tac tcc	2016
	Gln Ala Val Asp Tyr	Ile Lys Lys Leu Met	Thr Lys Gly Arg Tyr Ser	
		660	665	670
15	ctg gac gtg tgg agc			2031
	Leu Asp Val Trp Ser			
		675		

Figure 3 - Nucleotide and protein sequence of *Aspergillus ochraceus* oxidoreductase

5	cttatttcgt ttaggaagag caccggcttc ggtgtccttc cttaccctct tattcttctc	60
	cttctgactc cctttttgtt attgatcgcc catctcggtg aacatttggg atatctttcc	120
	ctctccccct cccgccccga ccttccttat cttctcctcc cgtccagcat ttagctcgcc	180
	atcgaattcg caattccttc ctcgtgactc ttcacgcgtg agcgtcctca tc atg gcg	238
	Met Ala	
10	caa ctc gat act ctc gat ttg gtc gtc ctg gtg gcg ctc ttg gtg ggt	286
	Gln Leu Asp Thr Leu Asp Leu Val Val Leu Val Ala Leu Leu Val Gly	
	5 10 15	
15	agc gtg gcc tac ttc acc aag ggc acc tac tgg gcc gtc gcc aaa gac	334
	Ser Val Ala Tyr Phe Thr Lys Gly Thr Tyr Trp Ala Val Ala Lys Asp	
	20 25 30	
20	cct tat gcc tcg gct ggt ccg gcg atg aat gga ggc gcc aag gcc gcc	382
	Pro Tyr Ala Ser Ala Gly Pro Ala Met Asn Gly Gly Ala Lys Ala Gly	
	35 40 45 50	
25	aag act cgc gac att gtt cag aaa atg gac gaa act ggc aaa aac tgt	430
	Lys Thr Arg Asp Ile Val Gln Lys Met Asp Glu Thr Gly Lys Asn Cys	
	55 60 65	
30	gtg att ttc tac ggc tcg caa acc ggt acc gct gag gac tac gcg tcc	478
	Val Ile Phe Tyr Gly Ser Gln Thr Gly Thr Ala Glu Asp Tyr Ala Ser	
	70 75 80	
35	aga ctg gcc aag gaa ggc tcc cag cga ttc ggt ctc aag acc atg gtg	526
	Arg Leu Ala Lys Glu Gly Ser Gln Arg Phe Gly Leu Lys Thr Met Val	
	85 90 95	
40	gcc gat ctg gag gac tac gac tac gaa aac ctg gaa aag ttc ccc gag	574
	Ala Asp Leu Glu Asp Tyr Asp Tyr Glu Asn Leu Glu Lys Phe Pro Glu	
	100 105 110	
45	gac aag gtt gtt ttc ttc gtt ctg gcc act tat ggc gag ggt gaa ccc	622
	Asp Lys Val Val Phe Phe Val Leu Ala Thr Tyr Gly Glu Gly Glu Pro	
	115 120 125 130	
50	acg gat aat cgc gtt gaa ttc tac cag ttc gtc acg ggc gaa gat gct	670
	Thr Asp Asn Ala Val Glu Phe Tyr Gln Phe Val Thr Gly Glu Asp Ala	
	135 140 145	
55	gct ttc gag agc ggc gct acc gcc gac gat aag cct ctg tct tct ctc	718
	Ala Phe Glu Ser Gly Ala Thr Ala Asp Asp Lys Pro Leu Ser Ser Leu	
	150 155 160	
60	aag tat gtc acg ttt ggt ctg ggt aac aac acc tat gag cac tac aac	766
	Lys Tyr Val Thr Phe Gly Leu Gly Asn Asn Thr Tyr Glu His Tyr Asn	
	165 170 175	
65	gct atg gtt cgc aat gtg gac gcc gct ctc aca aag ttc ggc gcc caa	814
	Ala Met Val Arg Asn Val Asp Ala Ala Leu Thr Lys Phe Gly Ala Gln	
	180 185 190	
70	cgc att ggc tct gct ggt gag ggt gac gac ggc gct ggt aca atg gaa	862
	Arg Ile Gly Ser Ala Gly Glu Gly Asp Asp Gly Ala Gly Thr Met Glu	
	195 200 205 210	
75	gag gat ttc ctg gcc tgg aag gaa ccc atg tgg gct gcc ctt tct gag	910
	Glu Asp Phe Leu Ala Trp Lys Glu Pro Met Trp Ala Ala Leu Ser Glu	
	215 220 225	
80	gcg atg aac ctg caa gag cgc gat gcg gtc tac gag ccg gtc ttc aat	958
	Ala Met Asn Leu Gln Glu Arg Asp Ala Val Tyr Glu Pro Val Phe Asn	
	230 235 240	
85	gtc acc gag gac gag tcc ctg agc ccc gaa gat gag aac gtt tac ctc	1006
	Val Thr Glu Asp Glu Ser Leu Ser Pro Glu Asp Glu Asn Val Tyr Leu	
	245 250 255	
90	ggg gag ccc act caa ggt cat ctc caa ggc gag ccc aag ggc ccg tac	1054
	Gly Glu Pro Thr Gln Gly His Leu Gln Gly Glu Pro Lys Gly Pro Tyr	
	260 265 270	

Figure 3, continued

5	tct gcg cac aac ccg ttc atc gct ccc atc tcc gaa tct cgt gaa ctg Ser Ala His Asn Pro Phe Ile Ala Pro Ile Ser Glu Ser Arg Glu Leu 275 280 285 290	1102
10	ttc aac gtc aag gac cgc aac tgt ctg cac atg gaa atc agc atc gcc Phe Asn Val Lys Asp Arg Asn Cys Leu His Met Glu Ile Ser Ile Ala 295 300 305	1150
15	ggt agc aac ctc act tac cag act ggt gac cac atc gct gtt tgg ccc Gly Ser Asn Leu Thr Tyr Gln Thr Gly Asp His Ile Ala Val Trp Pro 310 315 320	1198
20	acc aac gcc ggt tcc gag gtc gat cgg ttc ctg cag gct ttt ggt ctc Thr Asn Ala Gly Ser Glu Val Asp Arg Phe Leu Gln Ala Phe Gly Leu 325 330 335	1246
25	gaa gga aag cgc cac tcc gtc atc aac att aag ggt atc gat gtg acc Glu Gly Lys Arg His Ser Val Ile Asn Ile Lys Gly Ile Asp Val Thr 340 345 350	1294
30	gct aag gtt ccg att ccc act cct acg acc tat gac gcc gca gtt cgc Ala Lys Val Pro Ile Pro Thr Pro Thr Tyr Asp Ala Ala Val Arg 355 360 365	1342
35	tac tac ctg gaa gtc tgt gcc ccc gtt tcc cgt cag ttt gtc tcg act Tyr Tyr Leu Glu Val Cys Ala Pro Val Ser Arg Gln Phe Val Ser Thr 375 380 385	1390
40	ctc gct gcc ttt gcc cct gat gaa gcg acc aag gcg gag atc gtt cgt Leu Ala Ala Phe Ala Pro Asp Glu Ala Thr Lys Ala Glu Ile Val Arg 390 395 400	1438
45	ttg ggt ggc gac aag gac tat ttc cat gag aag att acc aac cga tgc Leu Gly Gly Asp Lys Asp Tyr Phe His Glu Lys Ile Thr Asn Arg Cys 405 410 415	1486
50	ttc aac atc gct cag gct ctc cag agc atc acg tcc aag cct ttc acc Phe Asn Ile Ala Gln Ala Leu Gln Ser Ile Thr Ser Lys Pro Phe Thr 420 425 430	1534
55	gcc gtc ccg ttc tcc ctg ctt atc gaa ggt atc acc aag ctt cag ccc Ala Val Pro Phe Ser Leu Leu Ile Glu Gly Ile Thr Lys Leu Gln Pro 435 440 445 450	1582
60	cgt tac tac tcg atc tcc tcg tct tcc ctg gtt cag aag gac aag att Arg Tyr Tyr Ser Ile Ser Ser Ser Ser Leu Val Gln Lys Asp Lys Ile 455 460 465	1630
65	agc att acc gcc gtt gtg gag tcg gtt cgc ttg cct ggt gag gaa cac Ser Ile Thr Ala Val Val Glu Ser Val Arg Leu Pro Gly Glu Glu His 470 475 480	1678
70	att gtc aag ggt gtg acc acg aac tat ctt ctc gcg ctc aag gaa aag Ile Val Lys Gly Val Thr Thr Asn Tyr Leu Leu Ala Leu Lys Glu Lys 485 490 495	1726
75	caa aac ggc gag cct tcc cct gac ccg cac ggc ttg act tac tct atc Gln Asn Gly Glu Pro Ser Pro Asp Pro His Gly Leu Thr Tyr Ser Ile 500 505 510	1774
80	act gga ccc cgt aac aag tac gat ggc atc cat gtc ccc gtt cac gtc Thr Gly Pro Arg Asn Lys Tyr Asp Gly Ile His Val Pro Val His Val 515 520 525 530	1822
85	cgc cac tcg aac ttc aaa ttg ccc tcg gat ccc tcg cga cct gtg atc Arg His Ser Asn Phe Lys Leu Pro Ser Asp Pro Ser Arg Pro Val Ile 535 540 545	1870
90	atg gtt gga ccc ggt act ggt gtt gct cct ttc cgt ggg ttt atc cag Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly Phe Ile Gln 550 555 560	1918
95	gag cgt gct gcc ttg gcc gcg aag ggc gag aag gtc gga act acc ttg Glu Arg Ala Ala Leu Ala Ala Lys Gly Glu Lys Val Gly Thr Thr Leu 565 570 575	1966
100	ctt ttc ttc ggc tgc cgt aag tcc gac gaa gat ttc ttg tac aag gat Leu Phe Phe Gly Cys Arg Lys Ser Asp Glu Asp Phe Leu Tyr Lys Asp 580 585 590	2014
105	gaa tgg aag act ttt cag gag cag ctt ggc gac tcg ctc aag atc atc	2062

Figure 3, continued

[illegible]

Figure 4 - Amino acid homology alignment of *A. ochraceus* 11 alpha hydroxylase with the top 10 BLAST hits from GenBank

5	CAA75565	1	---MANHSSSYHEFYKDHSTVL	LMSEKPVILPSLILGTCAVLLCIQWLK--	POPLIM					
	CAB91316	1	-----MERLDIKSI	LDPSATPFYSYLVTAFLAVVVS	SLQGPRF-PKNIKH					
	CAB56503	1	-----	LLFCFILSKTTKKGGNSQYS-	NHDELP					
	AAB94588	1	-----	MMVELHNHTPF	SIYFITSILFIFFVFKLVQRS--	DSKTS-STCKLP				
	pMON45624	1	-----	MPFFTGLLAIYHSLILDNPVQTLSTIVVLAAYT-	LATLQ--PSDLPE					
10	CAA75566	1	-----	MSIFNMITSYAG	QLLPFYIAIFVFTLVPAWIRSWLELRK-GSVVPL					
	AAD34552	1	---MTVDALTQPHHLLSLAWNDTQOHGSWFAPLVTT	SAGLLCLLLLCSSGR--	RSDLPV					
	CAA75567	1	-----	-----	-----					
	CAA76703	1	MSKSNSMNSTSHETLFQQLVLGLDRMPLMDVHWLIYVAFGAWLCS	VIHVLSSSSSTVKVP						
	CAA57874	1	-----	-----	-----					
CAA91268	1	-----	MALLILSLVISIFTFFIYIILARRER	KLREKIGLSGPEPH						
15	CAA75565	56	VNGRKFGELSNVFAARDFTFGAROLLEK	ELKMSPDKPFRIGT	VGEHITLPEKYAVEVRN					
	CAB91316	45	LNEKGPLEFSDTRPKKEFVYGSROLANWFKANPNKPCRVIS	DFGEATVILP	PMANETKN					
	CAB56503	28	PGEPQIPILGNAHQLSGGH-THH	IRDLKKYGPLMHLK-	IGEVSTIVASSEQIABETFR					
	AAB94588	45	PGERTLPLIGNIHQIVGSLPVHYIKNL	DKYGPLMHLN-LGEVSNLIVTS	REMAQETMK					
	pMON45624	46	LNEAKPFETNRRRVHEFVENS	KSILARRELHGHEPYRLS	EWGSLIVIPPECADELIN					
20	CAA75566	48	ANEPD-SLFGTGKTERSFVKLSRELLAKARSLFPNEPFLIT	EWGEVLIIP	PDFADETRN					
	AAD34552	56	FNEKTWWELTTMAARD	DANAPSWIESWFSQN-DKPI	EFVESGYCTLLPSSMADEFRK					
	CAA75567	1	-----	-----	-----					
	CAA76703	61	VVGYSRVFEPETWLL	SLRFVWEGGSITIGOSYNKFKDSIFQVRKLGTD	IVILPENYIDERRK					
	CAA57874	1	-----	-----	-----					
CAA91268	43	WFLGNLKQTAERKE	ELGVDANWFNHELHEQYGETFGIY-YGSQMN	EVISNEKDKIKYFI						
25	CAA75565	116	NEKES	TMAA--FKWFYAHLG	GFEG--FREGTNESH	IKLVARHQLT--HQLTLTGAVS				
	CAB91316	105	DDRUS	TRWT--YKAF	EGHLG	GFEG--FGEASRES	IIVOEVMRDLT--RYLNKYTEPLA			
	CAB56503	86	THDIL	ADRPSNLESPKIVSYD	SDMVVSPYGNVWQ	QPRKISMMELLSQESVQSFSIRE				
	AAB94588	104	THDINS	SDRP-DFVLS	RIVSNGSGIVFSQHGDYWFQ	PRKICTVELLTAKRQSFIRE				
	pMON45624	106	DPKMD	FETPT--TDDSH	GYL	GFDA-----LN-ADPN	IKVVTKYLT--KADNKTAPTIS			
30	CAA75566	107	DPRLS	SKAA--MQDN	EAGL	GFET--VALVGREDQL	QVARKQLT--KHSATIEPES			
	AAD34552	115	MKE	CMYKFLG--TDF	SHL	GFCDG--FKEVTRDAHL	ITRVVMNQFO--TQAPKYVKPLA			
	CAA75567	1	-----	-----	-----	-----	-----			
	CAA76703	121	LS	---	QDKTRSVEPFINDFACQYT--	RGMVFLQSDLQNS	VIQORLT--PKLVSTTKVMK			
	CAA57874	1	-----	-----	-----	-----	-----			
CAA91268	102	KNFSN	SDRS--VPSIYEANQLTASLLMNSYSSGW	HTRSAIPIF	SG--TGKMKAYQETIN					
35	CAA75565	170	E	CALV	PKDYTDSP--EWHDI	TAKDANKL	MARIISRV	ELCKENCPNOWERK--STYA		
	CAB91316	159	Q	TSMA	EANLPKAANGWSTIN	RSKIP	PIVARIS	RVELGEELCRNEEWIKVIT--QQYT		
	CAB56503	146	E	VLNF	IKSIG---SKEG-TR	INSKE	SLIT	YGLTRAAAFCEKNKNTETEFRLDQLTK		
	AAB94588	163	E	VAEL	KKHAATASEEGGSIFN	TQSTYS	MTFGIA	RAAAFCKKSRYQVFTSNMHKQLM		
	pMON45624	156	H	ASIA	KAVLGDDP--TWRE	TYPARDL	QLVAR	MSRVVEEGEENCNNDWQTS--SQYA		
40	CAA75566	161	R	STLA	SLNFGETT--EWR	ARRKPA	LDIL	ARISREYLDQLCRNEAWLKIT--KTYT		
	AAD34552	169	N	ASGI	ITDFGDSN--EWH	TPVYNQCL	LDVIT	TVFIMNCSKLAHNEEWLDIA--KHHA		
	CAA75567	17	M	KTS	FRWPTS-----	KWSSVS	YDMM	RTVALISGRAEVLPLICRLEGWLQAS--IGYT		
	CAA76703	173	E	LDYA	TKEMPDMKND	EWVEYD	SSIA	YRLISRTISARVVEPEHCKNOEWLTTI--AEYS		
	CAA57874	1	-----	-----	-----	-----	-----	-----		
CAA91268	159	S	KVDLF	EDIREKAS--SGQ	KWD	YDDFQGL	PLDMIGKCAFDISNCRNRNDVYFHPVT			
45	CAA75565	227	V	IAFRAVEEL	RLWF-SWLR	PWYQW	FPHCTQS	ALVQEP	RDENPTLTER-REBEK--AEA	
	CAB91316	218	H	DGFAAED	LRWF-AALR	PVHW	PLSCQ	RASAD	VRVRSITDPVKK--RQEK--AAN	
	CAB56503	202	A	VAEPNIAD	MFPSL-KFL	QLHST	SKYKIE	KIKHQ	FDVIVETILKGHKEINAPLS--QEN	
	AAB94588	223	E	LGGFSVAD	LYPSS-RV	FQM	GATG-KLEK	VHVT	DLQDIDEHK---MNRS--SEE	
	pMON45624	213	A	LAFGVGDK	LRWF-RH	RPVHW	FMFSC	WELRS	LRRCROLTPYTHK-RSLK--GTT	
50	CAA75566	218	T	NFYTASTN	LRWF-RS	IRP	PAHW	PLPECR	KLRQERKDAIGLITPLIER-REELT--RAA	
	AAD34552	226	V	TMAIQAR	QLRWF-VIL	RPVHW	LEPQ	AKHRAQ	VRRAQQLDPTIQE-RRAR--DAC	
	CAA75567	70	V	QCVSIRD	QLTWS-PHL	RPLIG	PELPS	VSRR	HLRPAELTAPLISQALODEKQHRAD	
	CAA76703	232	E	SFITG	FILR	VE-HIL	RPEI	APLPSY	RTLNRN	SSCRRVIGDILR---SQQ----
	CAA57874	1	-----	-----	-----	-----	-----	-----	-----	
CAA91268	217	E	KITIN	NFTYFHSSSPGTF	HFEST	LOIHTT	GC	RNSTCRRTYKCGFGFQDAKFCSDYE		
55	CAA75565	227	V	IAFRAVEEL	RLWF-SWLR	PWYQW	FPHCTQS	ALVQEP	RDENPTLTER-REBEK--AEA	
	CAB91316	218	H	DGFAAED	LRWF-AALR	PVHW	PLSCQ	RASAD	VRVRSITDPVKK--RQEK--AAN	
	CAB56503	202	A	VAEPNIAD	MFPSL-KFL	QLHST	SKYKIE	KIKHQ	FDVIVETILKGHKEINAPLS--QEN	
	AAB94588	223	E	LGGFSVAD	LYPSS-RV	FQM	GATG-KLEK	VHVT	DLQDIDEHK---MNRS--SEE	
	pMON45624	213	A	LAFGVGDK	LRWF-RH	RPVHW	FMFSC	WELRS	LRRCROLTPYTHK-RSLK--GTT	
60	CAA75566	218	T	NFYTASTN	LRWF-RS	IRP	PAHW	PLPECR	KLRQERKDAIGLITPLIER-REELT--RAA	
	AAD34552	226	V	TMAIQAR	QLRWF-VIL	RPVHW	LEPQ	AKHRAQ	VRRAQQLDPTIQE-RRAR--DAC	
	CAA75567	70	V	QCVSIRD	QLTWS-PHL	RPLIG	PELPS	VSRR	HLRPAELTAPLISQALODEKQHRAD	
	CAA76703	232	E	SFITG	FILR	VE-HIL	RPEI	APLPSY	RTLNRN	SSCRRVIGDILR---SQQ----
	CAA57874	1	-----	-----	-----	-----	-----	-----	-----	
CAA91268	217	E	KITIN	NFTYFHSSSPGTF	HFEST	LOIHTT	GC	RNSTCRRTYKCGFGFQDAKFCSDYE		
65	CAA75565	227	V	IAFRAVEEL	RLWF-SWLR	PWYQW	FPHCTQS	ALVQEP	RDENPTLTER-REBEK--AEA	
	CAB91316	218	H	DGFAAED	LRWF-AALR	PVHW	PLSCQ	RASAD	VRVRSITDPVKK--RQEK--AAN	
	CAB56503	202	A	VAEPNIAD	MFPSL-KFL	QLHST	SKYKIE	KIKHQ	FDVIVETILKGHKEINAPLS--QEN	
	AAB94588	223	E	LGGFSVAD	LYPSS-RV	FQM	GATG-KLEK	VHVT	DLQDIDEHK---MNRS--SEE	
	pMON45624	213	A	LAFGVGDK	LRWF-RH	RPVHW	FMFSC	WELRS	LRRCROLTPYTHK-RSLK--GTT	
70	CAA75566	218	T	NFYTASTN	LRWF-RS	IRP	PAHW	PLPECR	KLRQERKDAIGLITPLIER-REELT--RAA	
	AAD34552	226	V	TMAIQAR	QLRWF-VIL	RPVHW	LEPQ	AKHRAQ	VRRAQQLDPTIQE-RRAR--DAC	
	CAA75567	70	V	QCVSIRD	QLTWS-PHL	RPLIG	PELPS	VSRR	HLRPAELTAPLISQALODEKQHRAD	
	CAA76703	232	E	SFITG	FILR	VE-HIL	RPEI	APLPSY	RTLNRN	SSCRRVIGDILR---SQQ----
	CAA57874	1	-----	-----	-----	-----	-----	-----	-----	
CAA91268	217	E	KITIN	NFTYFHSSSPGTF	HFEST	LOIHTT	GC	RNSTCRRTYKCGFGFQDAKFCSDYE		

Figure 4, continued

5	CAA75565	283	ERTGEKV-TYNEAVEMLDDLAREK--GVGYDPACAQSLSSAA--LHSTHDFFTQVMFDH
	CAB91316	274	---GGKA-EHDDAIDPFERTA--K--SKYYDPAAQVLSIVA--LHTTSDLTCQVMNLI
	CAB56503	259	G--EKKE-DLVDVLLNIQRRNDFE--APLGDKNIKALIFNIFSAGTESSSTTQDWMCEM
	AAB94588	276	R--EAVE-DLVDVLLKFKQKES--E--FRLTDDNIKAVIQDIFIGGGETSSSVHEWMSSEL
	pMON45624	269	DEQCKPL-MFDESIEWFEREL-----GPNHDAVKQVILSTVA--LHTTSDDLLOAMSDI
10	CAA75566	274	IACQPLPVFHFAIDNSEQEAAAGTCASFDPVLFQILSLA--LHTTYDILLQQTVIDI
	AAD34552	282	RAKGIEPPRYVESTQWFEDTAK--CKWYDAAGAQIAEDFAC--LYGTSDDLIGSVVDI
	CAA75567	129	TLLADQTEGRGTFFISNLLRHLP--EELRTPQVGLDQMLSFAP--LHTTHMAITKVMWEL
	CAA76703	282	---GDGN---PILISNMRTAATGEE-KQIDNIAQRMILSLAS--LHTTAMTETHAMYDL
	CAA57874	44	--LEDPPTMLDHLNNGRNEHIA---DDVELQLHQTILAVE--TVTFISSTTOAYIDL
11	CAA91268	277	RRRCGEGSDSVLLKLLLNREDDKS-KPMTKQETIENCFIFLLAGYEITSTATYCSYLL
15	CAA75565	338	AQNPEITIEPLREEHIAVIGKQG-----ESKNSLYNKLMDSVLKESORLK--E-----
	CAB91316	324	QONPEITIEPLREEHIOVISEG-----EKTTSLYNKLMDSVLKESORVK--E-----
	CAB56503	314	IKNPTVMKKAQEEVRKVFNEBGN-----VDETKLHQLKYLQAVHKEITRLH--E-----
	AAB94588	329	IKNPTVMKKAQEEVRKVFYDSKGY-----VDETEHLQILYLKSLIKKEIMRLH--E-----
	pMON45624	321	AQNEKVLCAUREEVVRVISTEG-----LSKVSLSHSLKLDSDALKESORLE--E-----
20	CAA75566	332	GEHPEYIEPLREEVVQLREEG-----EKKTELFKKKLMDSDALKESORMK--E-----
	AAD34552	336	VNHPHLIEPLRDEIRTVIGQGG-----ETPASLYKLKLDSDALKESORVK--E-----
	CAA75567	186	VNRPEYIEPLRTEMQDVFQDPVSPDICINKERLSRLKLDSDALKESORWC--E-----
	CAA76703	333	CACPEYIEPLREVKSVYGASC-----EDKTAENRFKLDSDALKESORFN--E-----
	CAA57874	96	MAHPEYITLREEVESVPRDPNGN-----EIKDSTVAMDKLSDALKESORFNS--E-----
21	CAA91268	336	SKYENVOQKLYEETMEAKENG-----LTYDSIHNRKYLDCVYKETIRFY--E-----
30	CAA75565	384	-----IAIASMRRTFTTHVYKLSGCVIEPKNKLTIVSAHQHW-----DPEYVKK
	CAB91316	370	-----TGVASMRRYAERDMTSLDGTFTPKGQFVAVSAHDW-----NSEVHEQ
	CAB56503	361	-----PVPLLIFRECREQCKHK--GYTHPSKSEYIYNAAWAGR-----DPNYGIE
	AAB94588	376	-----PVPLLIFRVSRRERCOIN--GYELPSKTRIIYNAAWAGR-----NPKVYGE
	pMON45624	367	-----TLLGSRFRQATNDHKLKSGCVILKKGTIRVVIDSTHW-----NPEYVIT
35	CAA75566	378	-----GSIVIMRRYVTEDITLSSGLTLKKGTIRLVNDNRID-----DPKIMDN
	AAD34552	382	-----VECATMRSYALQVITFNGTFTPKGELVAAADRIS-----NPEVYPE
	CAA75567	238	-----STFVIPSFRVMKSMITLSNGIKLOEGTSTAFPAHMHMSEETPTTFSPFSSE
	CAA76703	379	-----VFLLAFNRIYHQSMTLSGDTNIPSGTIRIAPSAHLQ-----DSAHPVG
	CAA57874	152	KNYKLCESLTGHSNPTPTRTIADKKPDGTFYPKGTKEPENTCSHK-----DHKIMEN
36	CAA91268	382	-----PHFSFHRRLCRDITTHR--GQFYPKGATVCLPHTTHR-----NPEVADS
40	CAA75565	427	PLK-----FDGRRFFNVRREP--GKESKAQLVSATPDHMGFGYGLHACPGRRFASEIKI
	CAB91316	413	AEK-----ADGRRFLRRETTPGAGKENVAQLVSTAPCHGFGHGHACPGRRFAANEIKI
	CAB56503	404	PEK-----FNPDRFLS-----K---VDFKGNSEFYFPGGGRNICPGITFALANIEL
	AAB94588	419	TES-----EKPRFLNS-----S---IDFRGTDFFHFPFGAGRRNICPGITFALPNTIE
	pMON45624	410	PLQ-----ADGRRFFNKRQTP--GEDKNALLVSTISANHMGFGHGHACPGRRFASNEIKI
45	CAA75566	421	PEV-----GNPFRFYDMRSEA--GRDHGAQLVSTGSNHMGFGHGHACPGRRFAANEIKI
	AAD34552	425	PAK-----MDPFRFMRREDP--AKAFSAQLENTNGHMGFGWHFACPGRRFASKEIKI
	CAA75567	289	FENPSPRIEDGRRYLNHRSIK--GQGSQHQAATGFDYELIFNHGHACPGRRFAISEIKI
	CAA76703	423	FTP--PTBFDGRRMSKIRSDS--NYAQKYLFSMTDSSNMGFGYGYACPGRRFASNEIKI
	CAA57874	205	PEQ-----PDGTRFHKWRKAP--GREKRYMYSSSGTDLSHGFGRRHACPGRRFASAINIKI
46	CAA91268	425	PEE-----RHPRRFENWE-----E-----KSSSLKWLPGVGPFRYVGMRFAMERFKT
55	CAA75565	480	ALSHILLNYDEKPV-----EGSSMEPRKYCPNNANPTAKLSERRK--EEHAI-----
	CAB91316	468	ALVHLLNYEWRIP-----EGSDPKIRTFFSGVDFSLVEYKGRQ--PEHEL-----
	CAB56503	449	PLAQLLFFHEDWQS---NTEKLNKKE--SRGVYRREDDLYLTPVNFS--SSSPA-----
	AAB94588	464	PLAQLLFFHEDWKLPNKMKNEELDME--SNGHTLRQNDLCLIPITR-----TP-----
	pMON45624	463	ALCHILLNYEWRIP-----DGFKPQPLNIGTYLADPNTMLERPRK--AEIDMASLTV
60	CAA75566	474	ALCHILLNYDWKLC-----PDTETKPDTRCIAKSSPVTDLKRRRESVEDLEAI--
	AAD34552	478	MLAYLLNYDWKIV-----PDEPLQYRHSFSVRIHPTTILMLRRRD--EDIRLPGSL--
	CAA75567	347	ILIELLANYDEKLE-----DGKPGPELMRVCTETELDTKACLENRR-----
	CAA76703	479	TLAILLQDEERKLP-----DGKGRPRNITIDSDMIPLPRALCLNKR-----PRDE-----
	CAA57874	258	IKABLLNYDIKLP-----DGLSRPKNIEFEVLASLNACANA-----
61	CAA91268	468	TVVKLLDTTELKQF-----EGEADLIPOCNVILRRPNDPVRIHKKPRN-----
70	CAA75565	(SEQ ID NO: 27)	
	CAB91316	(SEQ ID NO: 28)	
	CAB56503	(SEQ ID NO: 29)	
	AAB94588	(SEQ ID NO: 30)	
	pMON45624	(SEQ ID NO: 02)	
75	CAA75566	(SEQ ID NO: 31)	
	AAD34552	(SEQ ID NO: 32)	
	CAA75567	(SEQ ID NO: 33)	
	CAA76703	(SEQ ID NO: 34)	
	CAA57874	(SEQ ID NO: 35)	
76	CAA91268	(SEQ ID NO: 36)	

Figure 5 - Phylogenetic tree showing the relatedness of *Aspergillus ochraceus* 11 alpha hydroxylase to the top 10 BLAST hits from GenBank

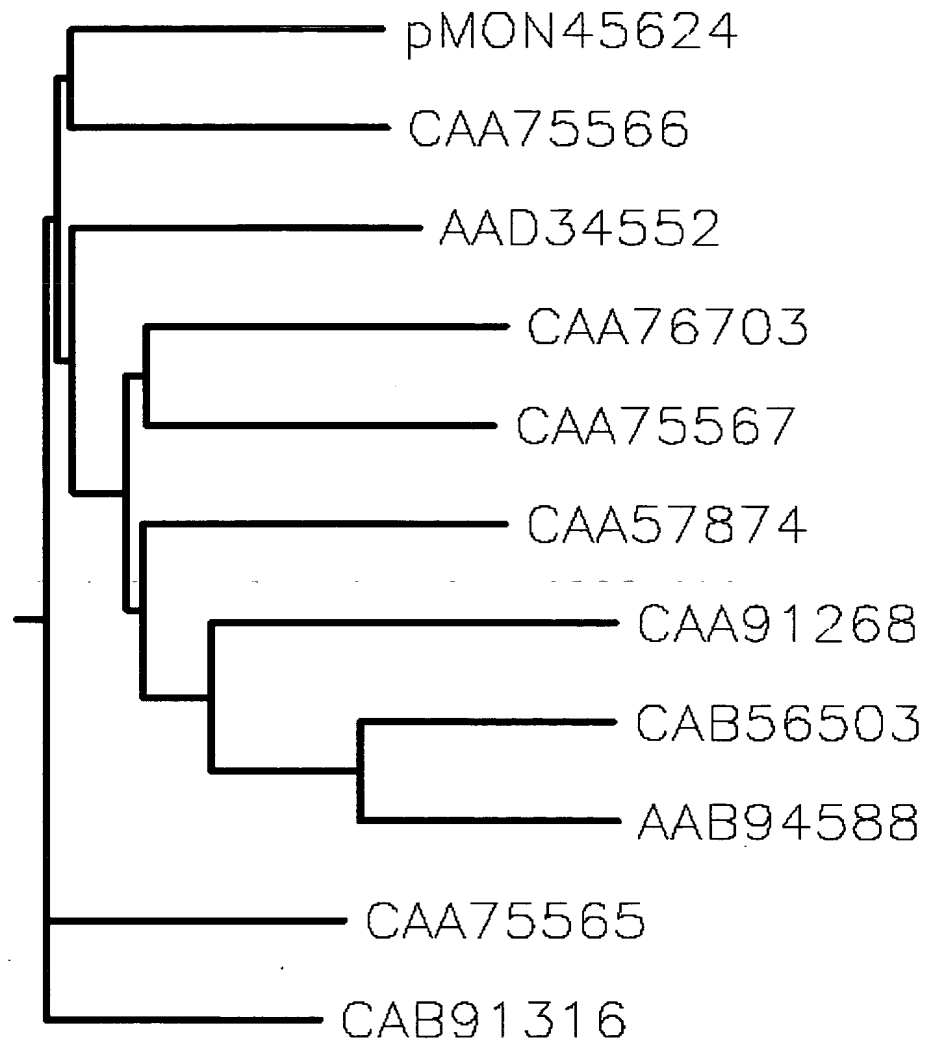


Figure 6 – Percent homology of *Aspergillus ochraceus* 11 alpha hydroxylase to the top 10 BLAST hits from GenBank

Accession Number	Species	% ID to 11a OH
CAB91316	<i>Neurospora crassa</i>	40
CAA76565	<i>Gibberella fujikuroi</i>	37
CAA75566	<i>Gibberella fujikuroi</i>	37
AAD34552	<i>Aspergillus terreus</i>	29
CAA75567	<i>Gibberella fujikuroi</i>	24
CAA57874	<i>Fusarium oxysporum</i>	24
CAA76703	<i>Gibberella fujikuroi</i>	23
CAB56503	<i>Catharanthus roseus</i>	14
AAB94588	<i>Glycine max</i>	14
CAA91268	<i>Caenorhabditis elegans</i>	12

Figure 7 – Amino acid homology alignment of *A. ochraceus* and human oxidoreductase to NADPH cytochrome P450 reductases from *A. niger*, mouse, and *S. cerevisiae*

5	PMON45605	1	MGDSHDTSSVSEAVAEVSLFSTDTMLFSLIVGLTYWFLFKKKEEPEFKIQTL
	human	1	MGDSHDTSSVSEAVAEVSLFSTDTMLFSLIVGLTYWFLFKKKEEPEFKIQTL
	mouse	1	MGDSHEDTSATVPEAVAEVSLFSTDTMLFSLIVGLTYWFLFKKKEEPEFSKIQT
	pMON45632	1	--MQDITLDDLVLVALLVGSAYFTKG-----TYWAAKDPYA--SAGPANGG
10	niger	1	--MQDITLDDLVLVALLVGSAYFTKG-----TYWAAKTPMP--LPAPENGA
	yeast	1	-MPFGDNDFTVLGLVLVLLYKRN-----SIKELMSDDG-----DIT-
15	PMON45605	61	TSSVRESSEVEKMKKTGRNIIVFGSQTGTAEHANRLSKD-AHRMGHRGMSADPEEYDL
	human	61	TSSVRESSEVEKMKKTGRNIIVFGSQTGTAEHANRLSKD-AHRMGHRGMSADPEEYDL
	mouse	61	APPVKESSEVEKMKKTGRNIIVFGSQTGTAEHANRLSKD-AHRMGHRGMSADPEEYDL
	pMON45632	47	AKRGKTRDIVKMDETGNCVIFFGSQTGTAEHANRLSKDREGGREGGRTMVADLEEYDY
20	niger	47	AKRGKTRNIEKMEETGNCVIFFGSQTGTAEHANRLSKDREGGREGGRTMVADLEEYDY
	yeast	42	AVSSGNRDIAVETENNNYIVLYSQTGTAEHAKKFSKELVAKNNVNMCADEVNYDF
25	PMON45605	120	ADLSSLPEIDNALVVFCMATYEGDPTDNAQDFYDLQ-----ET-----DVDLSGKKE
	human	120	ADLSSLPEIDNALVVFCMATYEGDPTDNAQDFYDLQ-----ET-----DVDLSGKKE
	mouse	120	ADLSSLPEIDKSLVVFCMATYEGDPTDNAQDFYDLQ-----ET-----DVDLSGKKE
	pMON45632	107	ENLEKFPEDK-VVFFVILATYEGEPDNAVVFYQFVTGEDAAEESGATADKPLSLKK
30	niger	107	ENLDQFPE-DK-VAFVFLATYEGEPDNAVVFYQFVTGDDVAFES-ASADKPLSLKK
	yeast	102	ESLNDMPV----IVSIFISTYEGEPDGAIVNFEDEHCN----AEAG-----ALSNERY
35	PMON45605	169	AVFGLGNKTYEHFNAMGKYVDKRLQQLGAQRI-FELGLGDD-DGNLEEDFITWEEQFWPAV
	human	169	AVFGLGNKTYEHFNAMGKYVDKRLQQLGAQRI-FELGLGDD-DGNLEEDFITWEEQFWPAV
	mouse	169	AVFGLGNKTYEHFNAMGKYVDKRLQQLGAQRI-FELGLGDD-DGNLEEDFITWEEQFWPAV
	pMON45632	165	VTFLGNNTYEHFNAMVNRVDAALTKFGAQRIGSAGEGDDGAGTTEEDFLAWKEPMAAL
40	niger	164	VAFGLGNNTYEHFNAMVROVDAAFKLGFORIGSAGEGDDGAGTTEEDFLAWKEPMAAL
	yeast	148	NVFLGNSTYEFNFAAKKAKHLSAAGATRLGKLGEDDAGACTTEEDFLAWKESILEV
45	PMON45605	228	CEHFGVEATGEESSIROQYELVVHTD----HDAKVYMGEMGRLSY-----ENQKP
	human	228	CEHFGVEATGEESSIROQYELVVHTD----HDAKVYMGEMGRLSY-----ENQKP
	mouse	228	CEHFGVEATGEESSIROQYELVVHTD----HDAKVYMGEMGRLSY-----ENQKP
	pMON45632	225	SEAMNIG---ERDAVYEPVFNVTEDSLSPEEDENVYLGEPQTQGLQ-----GEPKG
50	niger	224	SESMDFE---EREAVYEPVFNVTEDSLSPEEDENVYLGEPQTQGLQ-----GEPKG
	yeast	208	KDELHED---EEAKFTSDFQYTVLN---EITDSVSLGEPHSAHYLPESHQLNRRNADGIGLG
55	PMON45605	275	PFDAKNPFIAAATTNRKLNQGTERRHLMHLELDISDSKIRYESGDHVAVMPANDSALVNQL
	human	275	PFDAKNPFIAAATTNRKLNQGTERRHLMHLELDISDSKIRYESGDHVAVMPANDSALVNQL
	mouse	275	PFDAKNPFIAAATTNRKLNQGTERRHLMHLELDISDSKIRYESGDHVAVMPANDSTLVNQL
	pMON45632	273	PYSAHNPFTAPTESRELFTVKERNCHHETSIEGSLNYSYTGDDHIAVNPFTNAGAEVRF
60	niger	272	PYSAHNPFTAPTESRELFTVKERNCHHETSIEGSLNYSYTGDDHIAVNPFTNAGAEVRF
	yeast	262	PFLSLSPKTAFTVKSRELFTSSNERNCHHETSIEGSLNYSYTGDDHIAVNPFTNAGAEVRF
65	PMON45605	335	GKILGAD--LDVVMSLNNLDEESNKKHFPFCPTSYRTALTYYLEITNPRTNVLYELAQ
	human	335	GKILGAD--LDVVMSLNNLDEESNKKHFPFCPTSYRTALTYYLEITNPRTNVLYELAQ
	mouse	335	GEILGAD--LDVVMSLNNLDEESNKKHFPFCPTTYRTALTYYLEITNPRTNVLYELAQ
	pMON45632	333	LQAFGLGKRHSVFNKGED--VTAKVPIPTPTTYDAAVRYLYEYCAPVSRQFVSTLAAE
70	niger	332	LQAFGLGKRHSVFNKGED--VTAKVPIPTPTTYDAAVRYLYEYCAPVSRQFVSTLAAE
	yeast	322	LSIFNLD--PETTFDLKELD--PTVVPFPTPTTIGAAKHYLEITGVSRQFVSTLAAE
75	PMON45605	393	AS-EPSEQELLRKMSSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR
	human	393	AS-EPSEQELLRKMSSSGEGKELYLSWVVEARRHILAILQDCP-SLRPPIDHLCELLPR
	mouse	393	AS-EPSEQELLRKMSSSGEGKELYLSWVVEARRHILAILQDYP-SLRPPIDHLCELLPR
	pMON45632	391	APDEATKAEIVRLGCDKDYFHEKTNRCFNIAQ--ALQSETSKP-FTAVFSLIEGHTT
80	niger	390	APMRKARORLCVWLAQG-LFPFEGHQPMLOHAQ--ALQSETSKP-FSAVFSLIEGHTT
	yeast	378	APNADVKEKLTLLSKDKDQFVEVETSKYFNIAQ--ALKYISDGAKWDNVLEQFVSVFQ

Figure 7, continued

5	PMON45605	451	LQARYYSIASSSKVHPNSVHICAVVVEYETK---AGRINKGVATNWLRAKEP--AGE--
	human	451	LQARYYSIASSSKVHPNSVHICAVVVEYETK---AGRINKGVATNWLRAKEP--AGE--
	mouse	451	LQARYYSIASSSKVHPNSVHICAVVVEYETK---AGRINKGVATNWLRAKEP--AGE--
	PMON45632	448	LQARYYSIASSSLVQKCKISITAVVESVRLP---GEEHIVKGVITNILLALKEKQNGEPS
	niger	446	LQARYYSIASSSLVQKCKISITAVVESVRLP---GEEHIVKGVITNILLALKEKQNGERSL
10	yeast	436	HTPRYYSISSSSLSEKIVHHTSIVENFPNPELP-DAPPGVGVITNILLLENILAQNNVNI
	PMON45605	503	-----NGGR-----ALVPMFVRKSCFRLPFKAHTTPVIMVGPCTGVAPFIGFIQE
	human	503	-----NGGR-----ALVPMFVRKSCFRLPFKAHTTPVIMVGPCTGVAPFIGFIQE
	mouse	503	-----NGRR-----ALVPMFVRKSCFRLPFKAHTTPVIMVGPCTGVAPFMGFIQE
	PMON45632	505	PDPHG-LTYSITGPRNKVDGIHVPVHVRHSNFFLESDPSRPVIMVGPCTGVAPFRGFIQE
15	niger	503	SRPSR-LDLLHGGPRNKVDGIHVPVHVRHSNFFLESDPSRPVIMVGPCTGVAPFRGFIQE
	yeast	495	AETNLPVHYDLNGPRKLEANYKIPVHVRKSNFRLPSNPSTPVIMVGPCTGVAPFRGFIRE
20	PMON45605	547	RAWLRQ---QGKE---VGETLLMYGCRSDEDELYRDELAFQHRD-GALTQLNVAFSRE-
	human	547	RAWLRQ---QGKE---VGETLLMYGCRSDEDELYRDELAFQHRD-GALTQLNVAFSRE-
	mouse	547	RAWLRE---QGKE---VGETLLMYGCRSDEDELYRDELARFHRD-GALTQLNVAFSRE-
	PMON45632	564	RAALAA---KGEK---VGTTLLEFGCRSDEDELYKDEWKTEQEQLGDSLKITAFSRE-
	niger	562	RAALAA---KGEK---VGTTLLEFGCRSDEDELYKDEWKTEQEQLGDSLKITAFSRE-
25	yeast	555	RVAFLESQKKGGNNVSLGKHLLFYGSRNID-DELYQDEWPEYAKLDESFEVVAHSRLP
	PMON45605	599	QSHKVYVQHLLKQDREHFWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGMEHAQ
	human	599	QSHKVYVQHLLKQDREHFWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGMEHAQ
	mouse	599	QSHKVYVQHLLKQDREHFWKLI-EGGAHIYVCGDARNMARDVQNTFYDIVAELGMEHTC
	PMON45632	617	SAEKVYVQHRLREHSELVSDLL-KQKATFYVCGDAANMAREVNLVLGQTHAQRGLPAEK
30	niger	615	GPOKVYVQHRLREHSELVSDLL-KQKATFYVCGDAANMAREVNLVLGQTHAQRGLPAEK
	yeast	614	NTHKVYVQDKLRLEYEDQYFEMI-NNGAHIYVCGDAKGMARGVSTALVGLSRGKSHITDE
35	PMON45605	658	AVDYTKKLMTKGRYSLDVWS
	human	658	AVDYTKKLMTKGRYSLDVWS
	mouse	659	AVDYTKKLMTKGRYSLDVWS
	PMON45632	676	GEPMYKHHRRSGSYQDDVWS
	niger	674	GEPMYKHHRRSGRYQEDVWS
40	yeast	673	ATELIRMEKTSGRYQEDVW-
	PMON45605		(SEQ ID NO: 03)
	human		(SEQ ID NO: 06)
	mouse		(SEQ ID NO: 39)
	PMON45632		(SEQ ID NO: 05)
45	niger		(SEQ ID NO: 38)
	yeast		(SEQ ID NO: 37)

Figure 8 – Amino acid homology alignment of *A. ochraceus* oxidoreductase to NADPH cytochrome P450 reductases from *A. niger* and *S. cerevisiae*

5	<i>A. niger</i>	1	MAQLDTLDLVVLAVLLVGSVAYFTKGTYWAVAKTRMPLPFRMNGFAKAGKTRNITEKM
	<i>A. ochraceus</i>	1	MAQLDTLDLVVLAVLLVGSVAYFTKGTYWAVAKDPYASAEAMNGFAKAGKTRDIOMKM
	<i>S. cerevisiae</i>	1	MPFGEDNTLFTVLAEELVLAELVYVKRNSIKELMSDDCDITAVSSG-----NRDIAQVW
10	<i>A. niger</i>	60	ETGKNCVIFYGSOTGTAEDYASRLAKEGSORFGLKTMVADLEEYDYENLDOFPEDKVAF
	<i>A. ochraceus</i>	60	ETGKNCVIFYGSOTGTAEDYASRLAKEGSORFGLKTMVADLEEYDYENLEKFPEDKVVF
	<i>S. cerevisiae</i>	55	TENNKNYLVLVYFSOTGTAEDYAKKFKELVAKFNINVMCADMENYDEESLNDVPE--VIVS
15	<i>A. niger</i>	120	FVLATYGEGETDNAVIFYQFTGDDVAFES-ASADEKKPLSKLYVAFGLGNNTYEHYNA
	<i>A. ochraceus</i>	120	FVLATYGEGETDNAVIFYQFTGDDAFESCATADTKPLSSLYVTFGLGNNTYEHYNA
	<i>S. cerevisiae</i>	113	IFLSTYGEGETDCAVNFEDFEC-----NABAGALSNLRVNMFGLGNSITYEFHNE
20	<i>A. niger</i>	179	MVRNVDAAPKRLCEPORTGSAGEGDDGAGTMEEDFLAWKEPMWAALSESMLEEREAVVEF
	<i>A. ochraceus</i>	180	MVRNVDAAPKRLCEGAORIGSAGEGDDGAGTMEEDFLAWKEPMWAALSEAMNLOERFAVVEF
	<i>S. cerevisiae</i>	163	AARKAEKHLSEAGATIRCKLGEADDGAGTTDEDYNAWKESILEVLEKDEPHLECEAKETS
25	<i>A. niger</i>	239	VFCVTENESLSPEDENVYLGEPTQSHLQ-----GTPKGPYSAHNPFPIAPISEREL
	<i>A. ochraceus</i>	240	VFNVTEDSLSPEDENVYLGEPTQGHLO-----GTPKGPYSAHNPFPIAPISEREL
	<i>S. cerevisiae</i>	223	QFLVYI---VLNEITDSMSLGEPSAHYLPSSHQLNRNADGIQIGPFDLSQPHIAPIVKSEREL
30	<i>A. niger</i>	290	FNVKDRNCLHMEISTAGSNLSYOTGDHIAVWPTNAGAEVDRFLQAFGLEGRKDSVINIKG
	<i>A. ochraceus</i>	291	FNVKDRNCLHMEISTAGSNLSYOTGDHIAVWPTNAGAEVDRFLQAFGLEGRKDSVINIKG
	<i>S. cerevisiae</i>	280	FSSNDRNCHHSFDESSGNNKYSTGDHIAVWPSNPLEKVEQFLSIFENLEP--ETTFDDKP
35	<i>A. niger</i>	350	IDVTAKVPIPTPTTYDAAVRYVMEVCAPVSRQFVETLAAFAPMRKAEQRLCVWVAQG-LF
	<i>A. ochraceus</i>	351	IDVTAKVPIPTPTTYDAAVRYVLEVCAPVSRQFVSTLAAFAPDEATKAEIVRLCSDDKYF
	<i>S. cerevisiae</i>	338	EDPTVKVPPTPTPTIGAAKHYLEITTEPVSRQLFSLLIQFAPNADVKERLTLSKDKDOF
40	<i>A. niger</i>	409	PREGHSPLMAHAQALOSITS-KPFSAVPFSLLEGITKLOPRYYSISSSSLVOKDKISIT
	<i>A. ochraceus</i>	411	HEKITNRCFNIAQALOSITS-KPFSAVPFSLLEGITKLOPRYYSISSSSLVOKDKISIT
	<i>S. cerevisiae</i>	398	AVEITISKYFNIAQALOSITS-KPFSAVPFSLLEGITKLOPRYYSISSSSLVOKDKISIT
45	<i>A. niger</i>	468	AVVESVRLP--GASHYVKGVTNTNYLLALKKONGRSLSRFSR-LDLLHHGPRNKYDGIHV
	<i>A. ochraceus</i>	470	AVVESVRLP--GSEHYVKGVTNTNYLLALKKONGEPPSPDHG-LIYSHITGPRNKYDGIHV
	<i>S. cerevisiae</i>	458	STVENFPNPELPEAPPGVGVTTNLLRNHQLAQNNVNIAETNLPVHYDNGPRKLEANYKL
50	<i>A. niger</i>	525	PVHVRHSNFKLPSPSRPHIMVGPPTGVAPFRGFIQERAAALAAKGEK-----VGPTHLF
	<i>A. ochraceus</i>	527	PVHVRHSNFKLPSPSRPVIMVGPPTGVAPFRGFIQERAAALAAKGEK-----VGPTHLF
	<i>S. cerevisiae</i>	518	PVHVRHSNFKLPSPSPVIMVGPPTGVAPFRGFIRERVAFLSQKKGNNVSHGKHDLF
55	<i>A. niger</i>	579	FGCRKSDDEFLYKDEWKTYQDLGDNLKIIITAFSRE-GPOKVYVQHRLREHSELVSDLLK
	<i>A. ochraceus</i>	581	FGCRKSDDEFLYKDEWKTYQDLGDSLKIIITAFSRE-SAEKVYVQHRLREHSELVSDLLK
	<i>S. cerevisiae</i>	578	YGSRNIL-DFLYQDEWPEYAKRLDGSFEMVAHSRLPNTKVVYVCDLKEYEDQVFETIN
60	<i>A. niger</i>	638	OKATFYVCGDAANMAREVNLVLGQIIAORGLPAEKGEEMVKHMRGRYQEDVWS
	<i>A. ochraceus</i>	640	OKATFYVCGDAANMAREVNLVLGQIIAORGLPAEKGEEMVKHMRSCSYQEDVWS
	<i>S. cerevisiae</i>	637	NGAFIYVCGDAKGMAREVNLVLGQIIAORGLPAEKGEEMVKHMRSCSYQEDVW-
<i>A. ochraceus</i> , PMON45632 (SEQ ID NO: 05)			
<i>A. niger</i> (SEQ ID NO: 38)			
<i>S. cerevisiae</i> , yeast (SEQ ID NO: 37)			

Figure 9 – Phylogenetic tree showing the relatedness of Aspergillus ochraceus and human oxidoreductase to reductases from A. niger, yeast, and mouse.

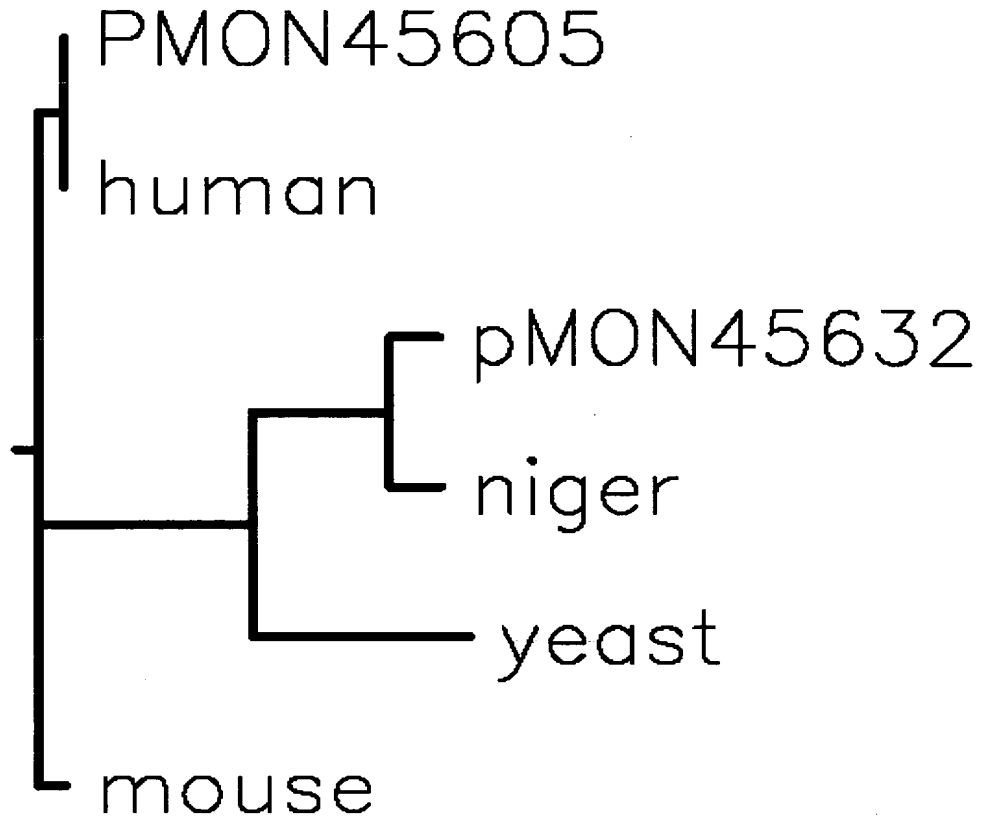


Figure 10 – Percent homology between Aspergillus ochraceus oxidoreductase to reductases from A. niger, yeast, and mouse and human.

Accession number	organism	% id to A.och oxred
CAA81550	<i>A. niger</i>	84
BAA02936	<i>S. cerevisiae</i>	37
BAA04496	mouse	34
AAB21814	human	33

Figure 11 – Amino acid homology alignment of human oxidoreductase with the top 4 hits from SwissProt

5	PMON45605	1	MGDSHVDTSSTVSEAVAEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEEVPEFHKIQTL
	human	1	MGDSHVDTSSTVSEAVAEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEEVPEFHKIQTL
	rabbit	1	MGDSHGDTGATEFEAAAEASMSMTDMVLFSLIVGLLTYWFLFRKKKEEVPEFHKIQAP
	rat	1	MGDSHEDTSATMFEAVAEVSLFSITDMVLFSLIVGLLTYWFLFRKKKEEVPEFHKIQTT
	mouse	1	MGDSHEDTSATMFEAVAEVSLFSITDMVLFSLIVGLLTYWFLFRKKKEEVPEFHKIQTT
10	pig	1	MGDSNVDTGTTSEMVAEVSLFSATDMVLFSLIVGLLTYWFLFRKKKDEVPEFSKIETT
	PMON45605	61	TSS-VRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	human	61	TSS-VRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	rabbit	61	TSS-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	rat	61	APP-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
15	mouse	61	APP-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
	pig	61	TSS-VKESFVEKMKKTGRNIIVFYGSQTGTAEFANRLSKDAHRYGMRGMSADPEEYDL
20	PMON45605	120	ADLSSLPEIDNALVVFCMATYGECDPTDNAQDFYDWLQETDVDLHGKFAVFGNGKNTYE
	human	120	ADLSSLPEIDNALVVFCMATYGECDPTDNAQDFYDWLQETDVDLHGKFAVFGNGKNTYE
	rabbit	121	ADLSSLPEIDNALVVFCMATYGECDPTDNAQDFYDWLQETDVDLHGKFAVFGNGKNTYE
	rat	120	ADLSSLPEIDKSLVVFCMATYGECDPTDNAQDFYDWLQETDVDLHGKFAVFGNGKNTYE
	mouse	120	ADLSSLPEIDKSLVVFCMATYGECDPTDNAQDFYDWLQETDVDLHGKFAVFGNGKNTYE
25	pig	120	ADLSSLPEIDNALVVFCMATYGECDPTDNAQDFYDWLQETDVDLHGKFAVFGNGKNTYE
30	PMON45605	180	HFNAMGKYVDKRLLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEE
	human	180	HFNAMGKYVDKRLLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEE
	rabbit	181	HFNAMGKYVDKRLLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEE
	rat	180	HFNAMGKYVDKRLLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEE
	mouse	180	HFNAMGKYVDKRLLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEE
35	pig	180	HFNAMGKYVDKRLLEQLGAQRIFELGLGDDDGNNLEEDFITWREQFWPAVCEHFGVEATGEE
	PMON45605	240	SSIROQYELVVHTDHLDAKVYMGEMGRKLSYENQKPPFDAKNPFLAAVTNNRKLNQGTERH
	human	240	SSIROQYELVVHTDHLDAKVYMGEMGRKLSYENQKPPFDAKNPFLAAVTNNRKLNQGTERH
	rabbit	241	SSIROQYELVHTDHLDAKVYMGEMGRKLSYENQKPPFDAKNPFLAAVTNNRKLNQGTERH
	rat	240	SSIROQYELVVHTDHLDAKVYMGEMGRKLSYENQKPPFDAKNPFLAAVTNNRKLNQGTERH
40	mouse	240	SSIROQYELVVHTDHLDAKVYMGEMGRKLSYENQKPPFDAKNPFLAAVTNNRKLNQGTERH
	pig	240	SSIROQYELVVHTDHLDAKVYMGEMGRKLSYENQKPPFDAKNPFLAAVTNNRKLNQGTERH
45	PMON45605	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGKILGADLDVVMISLNNLDEESNKKH
	human	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGKILGADLDVVMISLNNLDEESNKKH
	rabbit	301	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGADLDVVMISLNNLDEESNKKH
	rat	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGADLDVVMISLNNLDEESNKKH
	mouse	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGADLDVVMISLNNLDEESNKKH
50	pig	300	LMHLELDISDSKIRYESGDHVAVYPANDSALVNQLGEILGADLDVVMISLNNLDEESNKKH
	PMON45605	360	PPCPCTSYRTALTYVLDITNPPTNVLVELAQYASEPSEQELLRKMASSSGEGKELYLSW

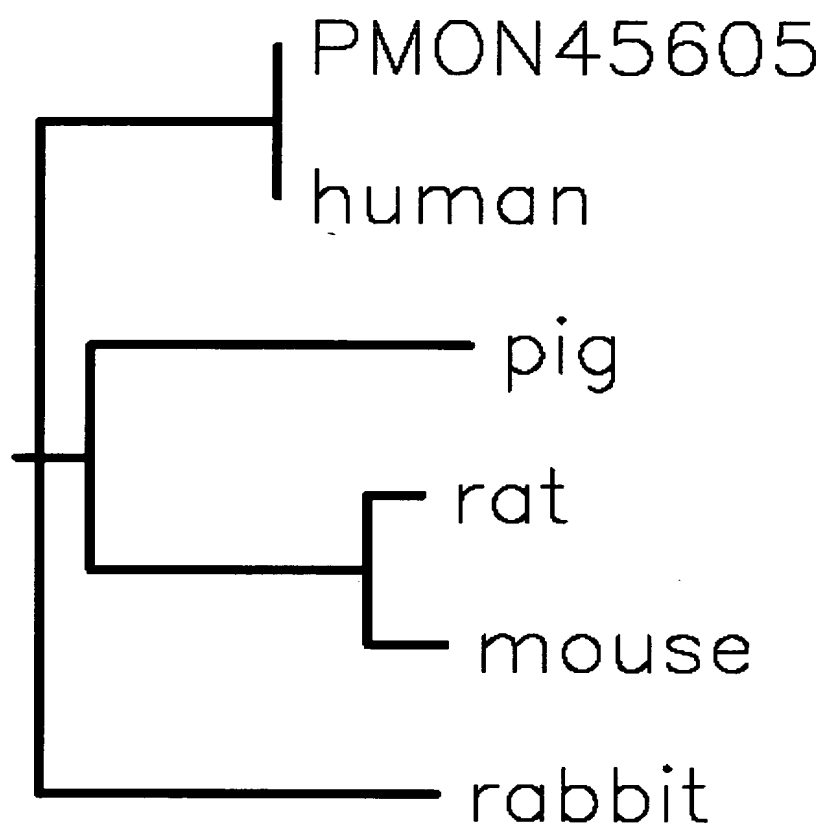
Figure 11, continued

5	PMON45605	360	PFPCPTSYRTALTYTYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
	human	360	PFPCPTSYRTALTYTYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
	rabbit	361	PFPCPTSYRTALTYTYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
	rat	360	PFPCPTSYRTALTYTYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
	mouse	360	PFPCPTSYRTALTYTYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
	pig	360	PFPCPTSYRTALTYTYLDITNPPRTNVLYELAQYASEPSEQELLRKMASSSGEGKELYLSW
10	PMON45605	420	VVEARRHILAILQDCPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
	human	420	VVEARRHILAILQDCPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
	rabbit	421	VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
	rat	420	VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
	mouse	420	VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
15	pig	420	VVEARRHILAILQDYPSLRPPIDHLCCELLPRLQARYYSIASSSKVHPNSVHICAVVVEYE
20	PMON45605	480	TKAGRNKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVA
	human	480	TKAGRNKGVATNWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVA
	rabbit	481	TKAGRNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVA
	rat	480	AKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVA
	mouse	480	AKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVA
	pig	480	TKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQFRLPFKATTPVIMVGPGTGVA

Figure 11, continued

5	PMON45605	540	FIGFIQERAWLRQOGKEVGETLLYYGCRRSDEDYLYREELAQFHFDGALTQLNVAFSREQ
	human	540	FIGFIQERAWLRQOGKEVGETLLYYGCRRSDEDYLYREELAQFHFDGALTQLNVAFSREQ
	rabbit	541	FIGFIQERAWLRQOGKEVGETLLYYGCRRSDEDYLYREELAQFHFDGALTQLNVAFSREQ
	rat	540	FIGFIQERAWLRQOGKEVGETLLYYGCRRSDEDYLYREELARFHKDGALTQLNVAFSREQ
	mouse	540	FIGFIQERAWLRQOGKEVGETLLYYGCRRSDEDYLYREELARFHKDGALTQLNVAFSREQ
	pig	540	FIGFIQERAWLRQOGKEVGETLLYYGCRRSDEDYLYREELAQFHAKGALTQLNVAFSREQ
10	PMON45605	600	SHKVYVQHLLKQDSEHLWKLI-EGGAHIYVCGDARNMARDVQNTFFYDIVAELGMEHAQA
	human	600	SHKVYVQHLLKQDSEHLWKLI-EGGAHIYVCGDARNMARDVQNTFFYDIVAELGMEHAQA
	rabbit	601	SHKVYVQHLLKQDSEHLWKLI-EGGAHIYVCGDARNMARDVQNTFFYDIVAELGMEHAQA
	rat	600	AHKVYVQHLLKRDSEHLWKLIHEGGAHIYVCGDARNMARDVQNTFFYDIVAELGMEHAQA
	mouse	600	AHKVYVQHLLKRDSEHLWKLIHEGGAHIYVCGDARNMARDVQNTFFYDIVAELGMEHAQA
15	pig	600	POKVVYVQHLLKRDSEHLWKLIHEGGAHIYVCGDARNMARDVQNTFFYDIVAELGMEHAQA
20	PMON45605	659	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 03)
	human	659	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 52)
	rabbit	661	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 53)
	rat	660	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 54)
	mouse	660	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 55)
	pig	660	VDYVKKLMTKGRYSLDVWS (SEQ ID NO: 56)

Figure 12 – Phylogenetic tree showing the relatedness of human oxidoreductase (P16435) with top 4 hits from SwissProt



***Figure 13 – Percent homology between human oxidoreductase and top 4 hits
from SwissProt***

Accession number	Species	% id to human oxred
P00388	rat	92
P00389	rabbit	92
P37040	mouse	92
P04175	pig	91

Figure 14 - Expression of Aspergillus ochraceus 11 alpha hydroxylase in transfected Sf9 insect cells

Expression of 11- α -Hydroxylase in Transfected Sf9 Cells

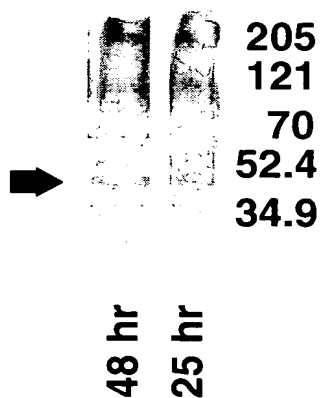


Figure 15 - Expression of Aspergillus ochraceus P450 oxidoreductase in transfected Sf9 insect cells

Expression of Fungal P-450 Oxidoreductase in Transfected Sf9 Cells

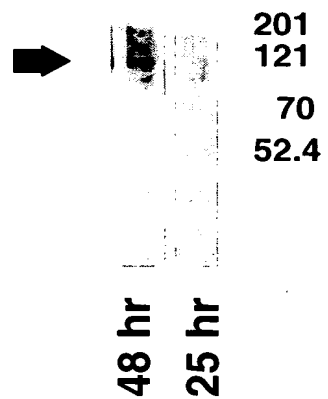


Figure 16 - Conversion of androstenedione to 11 alpha hydroxy androstenedione monitored by HPLC

